



PCT09

RAW SEQUENCE LISTING

DATE: 06/06/2002

PATENT APPLICATION: US/09/913,655

TIME: 13:16:28

Input Set : A:\BC1003 PCT Seq Listing.txt

Output Set: N:\CRF3\06062002\I913655.raw

p.6

3 <110> APPLICANT: E. I. du Pont de Nemours and Company
5 <120> TITLE OF INVENTION: Homologs of MAR-binding Filament-like protein 1 (MFPL)
7 <130> FILE REFERENCE: BC1003 PCT
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C--> 10 <141> CURRENT FILING DATE: 2002-01-17
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13 <151> PRIOR FILING DATE: 1999-04-12
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20 <211> LENGTH: 2168
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27 aagaaaatgc cagctatggc atgtatacac tcggagaatc aaaaggaaag cgaattctgc 180
28 agcagaagaa cgattctttt cgtgggtttc tctgttcttc cacttctcag cttgagggca 240
29 aatgcttttg aaggcttgtc agtagattct caagtaaaag cacagccgca gaaagaggag 300
30 acagagcaaa caatccaagg aaatgcagag aatcccttct tttctctact taatggactt 360
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33 gtttcatgga gaagaaattc cagtctgagc tgctgaacga aagggatata cgaaataatc 540
34 aacttaagag ggcaggcgaa gaacggcaag ctctggttaa ccaattgaat tcagcaaaga 600
35 gtacagtaac taaccttggc caggagctgc aaaaagaaaa acgaattgct gaagagctca 660
36 tagttcagat cgagggcctt caaaataacc tcatgcagat gaaggaggat aagaaaaaat 720
37 tgcaggagga gcttaaagag aagcttgatt tgatacaagt tctgcaagaa aagataactt 780
38 tacttactac agagatcaaa gataaagagg catctcttca gagtacaacc tctaaactag 840
39 ctgaaaaaga atcagaggta gataaattga gctcaatgta tcaggaaatcc caggatcagc 900
40 tgatgaattt gacttcagaa atcaaagaac ttaaagtcga agtccagaaa agagagagag 960
41 aactagagtt gaaacgtgaa tcagaagaca accttaatgt gcgattaaat tctttgctcg 1020
42 ttgagagaga tgaatctaaa aaagagcttg atgctattca aaaggaatac agcgagttca 1080
43 agtccatttc agagaagaaa gtggcctctg atgccaagct gttgggggaa caagaaaaga 1140
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48 agcttgaagc tgagggttct aaacttcaga tgggaattgga ggaaacaaga acatcattac 1440
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ENTERED

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56 aaaagtctgt ttctgagcag aaacaaattt ctcaagaatc ccgagaaaac cttgaagatg 1920
57 cccatagcct ggtaatgaaa cttggcaagg aacgcgagag tctggagaag agagcaaaga 1980
58 aattggaaga tgaaatggca tcagcaaaag gtgagatttt gcggctgcgg acccaagtaa 2040
59 attcggtaaa agctcctgtt aacaatgagg aaaaagttga agctggggaa aaggcagctg 2100
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72 Ser Ser Ser Ser Ile Ser Ser Ser Gln Phe Thr Pro Leu Leu Phe Ser
73 20 25 30
75 Pro Arg Asn Ala Gln Lys Cys Lys Lys Lys Met Pro Ala Met Ala Cys
76 35 40 45
78 Ile His Ser Glu Asn Gln Lys Glu Ser Glu Phe Cys Ser Arg Arg Thr
79 50 55 60
81 Ile Leu Phe Val Gly Phe Ser Val Leu Pro Leu Leu Ser Leu Arg Ala
82 65 70 75 80
84 Asn Ala Phe Glu Gly Leu Ser Val Asp Ser Gln Val Lys Ala Gln Pro
85 85 90 95
87 Gln Lys Glu Glu Thr Glu Gln Thr Ile Gln Gly Asn Ala Glu Asn Pro
88 100 105 110
90 Phe Phe Ser Leu Leu Asn Gly Leu Gly Val Phe Gly Ser Gly Val Leu
91 115 120 125
93 Gly Ser Leu Tyr Ala Leu Ala Arg Asn Glu Lys Ala Val Ser Asp Ala
94 130 135 140
96 Thr Ile Glu Ser Met Lys Asn Lys Leu Lys Glu Lys Glu Ala Thr Phe
97 145 150 155 160
99 Val Ser Met Glu Lys Lys Phe Gln Ser Glu Leu Leu Asn Glu Arg Asp
100 165 170 175
102 Ile Arg Asn Asn Gln Leu Lys Arg Ala Gly Glu Glu Arg Gln Ala Leu
103 180 185 190
105 Val Asn Gln Leu Asn Ser Ala Lys Ser Thr Val Thr Asn Leu Gly Gln
106 195 200 205
108 Glu Leu Gln Lys Glu Lys Arg Ile Ala Glu Glu Leu Ile Val Gln Ile
109 210 215 220
111 Glu Gly Leu Gln Asn Asn Leu Met Gln Met Lys Glu Asp Lys Lys Lys
112 225 230 235 240
114 Leu Gln Glu Glu Leu Lys Glu Lys Leu Asp Leu Ile Gln Val Leu Gln
115 245 250 255
117 Glu Lys Ile Thr Leu Leu Thr Thr Glu Ile Lys Asp Lys Glu Ala Ser
118 260 265 270
120 Leu Gln Ser Thr Thr Ser Lys Leu Ala Glu Lys Glu Ser Glu Val Asp
121 275 280 285

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129 Glu Leu Glu Leu Lys Arg Glu Ser Glu Asp Asn Leu Asn Val Arg Leu
130      325      330      335
132 Asn Ser Leu Leu Val Glu Arg Asp Glu Ser Lys Lys Glu Leu Asp Ala
133      340      345      350
135 Ile Gln Lys Glu Tyr Ser Glu Phe Lys Ser Ile Ser Glu Lys Lys Val
136      355      360      365
138 Ala Ser Asp Ala Lys Leu Leu Gly Glu Gln Glu Lys Arg Leu His Gln
139      370      375      380
141 Leu Glu Glu Gln Leu Gly Thr Ala Ser Asp Glu Val Arg Lys Asn Asn
142 385      390      395      400
144 Val Leu Ile Ala Asp Leu Thr Gln Glu Lys Glu Asn Leu Arg Arg Met
145      405      410      415
147 Leu Asp Ala Glu Leu Glu Asn Ile Ser Lys Leu Lys Leu Glu Val Gln
148      420      425      430
150 Val Thr Gln Glu Thr Leu Glu Lys Ser Arg Ser Asp Ala Ser Asp Ile
151      435      440      445
153 Ala Gln Gln Leu Gln Gln Ser Arg His Leu Cys Ser Lys Leu Glu Ala
154      450      455      460
156 Glu Val Ser Lys Leu Gln Met Glu Leu Glu Glu Thr Arg Thr Ser Leu
157 465      470      475      480
159 Arg Arg Asn Ile Asp Glu Thr Lys Arg Gly Ala Glu Leu Leu Ala Ala
160      485      490      495
162 Glu Leu Thr Thr Thr Arg Glu Leu Leu Lys Lys Thr Asn Glu Glu Met
163      500      505      510
165 His Thr Met Ser His Glu Leu Ala Ala Val Thr Glu Asn Cys Asp Asn
166      515      520      525
168 Leu Gln Thr Glu Leu Val Asp Val Tyr Lys Lys Ala Glu Arg Ala Ala
169      530      535      540
171 Asp Glu Leu Lys Gln Glu Lys Asn Ile Val Val Thr Leu Glu Lys Glu
172 545      550      555      560
174 Leu Thr Phe Leu Glu Ala Gln Ile Thr Arg Glu Lys Glu Ser Arg Lys
175      565      570      575
177 Asn Leu Glu Glu Glu Leu Glu Arg Ala Thr Glu Ser Leu Asp Glu Met
178      580      585      590
180 Asn Arg Asn Ala Phe Ala Leu Ala Lys Glu Leu Glu Leu Ala Asn Ser
181      595      600      605
183 His Ile Ser Ser Leu Glu Asp Glu Arg Glu Val Leu Gln Lys Ser Val
184      610      615      620
186 Ser Glu Gln Lys Gln Ile Ser Gln Glu Ser Arg Glu Asn Leu Glu Asp
187 625      630      635      640
189 Ala His Ser Leu Val Met Lys Leu Gly Lys Glu Arg Glu Ser Leu Glu
190      645      650      655
192 Lys Arg Ala Lys Lys Leu Glu Asp Glu Met Ala Ser Ala Lys Gly Glu
193      660      665      670
195 Leu Arg Leu Arg Thr Gln Val Asn Ser Val Lys Ala Pro Val Asn Asn

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208 <211> LENGTH: 1199
209 <212> TYPE: DNA
210 <213> ORGANISM: Nicotiana tabacum
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215 cagagaagag agtggcttca gatgccaaagc tggtggggga acaagaaaag agactacacc 180
216 agctcgagga acaacttggg actgccgtaa gtgaagtaag aaaaaataaa gtgctaattg 240
217 ctaatttgac tcaagcaaaa gaaaacctaa ggagaatgct ggacgctgag ctggaaaatg 300
218 taagcaagtt gaagctagag gtccaggtta ctccaggaaac tcttgagaaa tcaagaagtg 360
219 aagcttctga tatagtagaa caactacagc agtcgaggca cttgtgctct aagcttgaag 420
220 ctgaggtttc taagcttcag atggaattgg aggaaacaag gacattgtta cagaagaaca 480
221 ttgatgagac aaaacgtggt gcagagttct tagctgcgga gctgaccact actagggagc 540
222 ttctaaagaa aacaaatgaa gaaatgcaca ccatatccaa tgaactagct gctgttactg 600
223 aaaatcgtga taacttacag acggagctag ttgatgtcta caagaaagca gaacgtgctg 660
224 ttaatgaact gaaacaagaa aagaatattg tcgtgacatt ggagaaagag ctaacatttt 720
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226 gggctacaga atcacttgat gagatgaaca gaaatgcttt tgcacttgca aaggagctgg 840
227 agctcgctaa ttctcgtatt tctagcctca aagacgagag agaagtgctc caaaagtctg 900
228 tttctgagca gaagcaaatt tctcaagaag cccgagaaaa ccttgaagat gcccatagcc 960
229 tgggtgatgaa acttggcaag gaacgcgaga gtctggagaa gagagcaaag aaattggaag 1020
230 atgaaatggc atcagcaaaa ggtgagattt tgcggttgcg gacacaagta aattcggtaa 1080
231 aagctcctgt taacaaagag gaaaaagttg aagctgggga aaaggcaaca gtaacagtga 1140
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235 <211> LENGTH: 398
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244          20          25          30
246 Tyr Ser Glu Phe Lys Ser Ile Ser Glu Lys Arg Val Ala Ser Asp Ala
247          35          40          45
249 Lys Leu Leu Gly Glu Gln Glu Lys Arg Leu His Gln Leu Glu Glu Gln
250          50          55          60
252 Leu Gly Thr Ala Val Ser Glu Val Arg Lys Asn Lys Val Leu Ile Ala
253 65          70          75          80
255 Asn Leu Thr Gln Ala Lys Glu Asn Leu Arg Arg Met Leu Asp Ala Glu
256          85          90          95
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265          130          135          140
267 Leu Gln Met Glu Leu Glu Glu Thr Arg Thr Leu Leu Gln Lys Asn Ile
268 145          150          155          160
270 Asp Glu Thr Lys Arg Gly Ala Glu Leu Leu Ala Ala Glu Leu Thr Thr
271          165          170          175
273 Thr Arg Glu Leu Leu Lys Lys Thr Asn Glu Glu Met His Thr Ile Ser
274          180          185          190
276 Asn Glu Leu Ala Ala Val Thr Glu Asn Arg Asp Asn Leu Gln Thr Glu
277          195          200          205
279 Leu Val Asp Val Tyr Lys Lys Ala Glu Arg Ala Val Asn Glu Leu Lys
280          210          215          220
282 Gln Glu Lys Asn Ile Val Val Thr Leu Glu Lys Glu Leu Thr Phe Leu
283 225          230          235          240
285 Glu Ala Gln Ile Thr Arg Glu Lys Glu Ser Pro Lys Asn Leu Glu Glu
286          245          250          255
288 Glu Leu Glu Arg Ala Thr Glu Ser Leu Asp Glu Met Asn Arg Asn Ala
289          260          265          270
291 Phe Ala Leu Ala Lys Glu Leu Glu Leu Ala Asn Ser Arg Ile Ser Ser
292          275          280          285
294 Leu Lys Asp Glu Arg Glu Val Leu Gln Lys Ser Val Ser Glu Gln Lys
295          290          295          300
297 Gln Ile Ser Gln Glu Ala Arg Glu Asn Leu Glu Asp Ala His Ser Leu
298 305          310          315          320
300 Val Met Lys Leu Gly Lys Glu Arg Glu Ser Leu Glu Lys Arg Ala Lys
301          325          330          335
303 Lys Leu Glu Asp Glu Met Ala Ser Ala Lys Gly Glu Ile Leu Arg Leu
304          340          345          350
306 Arg Thr Gln Val Asn Ser Val Lys Ala Pro Val Asn Lys Glu Glu Lys
307          355          360          365
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317 <212> TYPE: DNA
318 <213> ORGANISM: Lycopersicon esculentum
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323 agaatcggag gtaaatagtt tgagcgatat gtatcaacaa tcccaggatc agctgatgaa 180
324 tttagacttca gagatcaaag aacttaaaga tgaaatccag aaaagagaga gagaactgga 240
325 gttgaaatgt gtatcagaag acaacctgaa tgtgcaatta aattctttgc tcctcgagag 300
326 agatgaatct aaaaaagagc ttcatgctat tcaaaaggaa tacagtgagt tcaagtccaa 360
327 ttctgatgag aaggtggcct cagatgcgaa gctgttgggg gaacaagaga agagactaca 420

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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 06/06/2002
PATENT APPLICATION: US/09/913,655 TIME: 13:16:29

Input Set : A:\BC1003 PCT Seq Listing.txt
Output Set: N:\CRF3\06062002\I913655.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:23; N Pos. 305
Seq#:24; Xaa Pos. 102